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CancerAI: A Deep Learning Framework for Ovarian Cancer Prediction

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Abstract— **Ovarian cancer is the fifth most common cause of death from cancer in women. This is mainly because it is often diagnosed at a late stage, as the earliest symptoms are unclear and inconsistent. Existing diagnostic techniques, such as biomarkers, biopsies, and imaging tests, have notable drawbacks such as reliance on subjective interpretation, inconsistency across different observers, and time-consuming testing procedures. This research study introduces an innovative deep learning framework that employs a convolutional neural network (CNN) algorithm to accurately predict and diagnose ovarian cancer, thereby overcoming the existing constraints. The CNN was trained using a dataset of histopathology images. The dataset was partitioned into test and training subsets to enhance the model's performance. The algorithm demonstrated an impressive accuracy rate of 96%, successfully detecting 97.12% of malignant instances and precisely categorizing 95.02% of healthy cells. This method effectively mitigates the challenges related to human expert evaluation, including elevated rates of misclassification and variability across different observers, while also reducing the time required for analysis. The results underscore the capability of this CNN-based technique to offer a more precise, effective, and dependable strategy for forecasting and detecting ovarian cancer. Subsequent investigations will prioritize the integration of new breakthroughs in deep learning to further amplify the efficacy of the suggested approach.**

Keywords— Deep Learning, Prediction, Ovarian Cancer, Convolution neural network

I. INTRODUCTION

Ovarian cancer has an annual death rate of 151,900, making it the most lethal malignancy worldwide [1]. Miller reports that it is the sixth leading cause of mortality among women. Ovarian cancer is the most prevalent form of gynaecological carcinoma, originating from epithelial tissue. This kind accounts for 90% of all occurrences. Clear-cell cancer of the ovary (C-COC), high-grade saline ovary cancers (H-GS-OC), low-grade saline ovary cancer (L-GS-OC), and endometrioid ovary cancer (E-O-C) are the five histologic carcinomas. Mucinous ovary cancers (M-OC) is the most common kind of ovarian cancer. These cancers have a bleak prognosis when diagnosed at an advanced stage [2].

Ferraro et al. [3] found that individuals who take oral contraceptives had lower levels of HE4 ($p = 0.008$). Biopsy, ultrasound imaging CAT (CT), electromagnetic resonance imaging, and PET (positron emission tomography), combined with novel techniques for training deep CNN, have shown great precision in forecasting and diagnosing seriously epithelial cells ovarian cancer.

There are some diagnostic methods for ovarian cancer include biomarkers, biopsies, and imaging tests

Biomarkers: CA-125 biomarkers are commonly employed for the detection of ovarian cancer. Nevertheless, their ability to accurately identify and detect conditions, particularly in the first phases, is restricted. This frequently leads to incorrect positive findings, which can result in unneeded procedures, or incorrect negative results, where the presence of cancer goes undiscovered until it has reached an advanced stage. Elevated CA-125 levels can also occur in benign illnesses including infertility and pelvic inflammation, which might complicate its reliability as a diagnostic tool.

Biopsies: Biopsies involve the microscopic examination of tissue samples and are considered the gold standard for cancer diagnosis. However, the process is invasive and subject to human interpretation, introducing variability and subjectivity. Different pathologists may interpret the same biopsy differently, leading to inconsistent results. Additionally, the invasive nature of biopsies can cause

discomfort and anxiety for patients, and there is a risk of complications such as infection and bleeding.

Imaging Tests: Imaging techniques such as ultrasound, MRI, and CT scans are crucial for visualizing tumours and assessing their spread. However, these tests rely heavily on the skill and experience of the radiologist. The subjective nature of image interpretation can lead to varying diagnoses among different practitioners. Additionally, these methods can be time-consuming and resource-intensive. Ultrasound, while non-invasive, can be limited by the operator's experience and the patient's anatomy. MRI and CT scans, although more detailed, are expensive and not always readily available, especially in resource-limited settings.

Cell tumour prognosis and therapy depend on accurate prediction and diagnosis, improving patient outcomes. Deep learning has various advantages:

- Handling Large Datasets: Deep learning processes large datasets and makes accurate predictions, reducing misdiagnosis.
- Deep learning detects ovarian cancer early, improving treatment success.
- Personalized therapy: Deep learning algorithms anticipate therapy responses, making care more efficient and individualized.

DeepOva, a deep learning system for cell tumour prediction and diagnostics, is introduced in this research. The framework efficiently analyzes the pictures in less than 5 seconds, achieving a result score of 0.95 with the utilization of advanced approaches. Related work, materials and techniques, findings and discussion, and conclusions are organized. DeepOva, advances tumour diagnosis, improving patient treatment and outcomes.

II. RELATED WORK

Several advanced deep-learning methods have been researched to categorize ovarian cancer according to the specific cell type. Accurate identification of the specific kind of ovarian cancer is crucial for developing personalized treatment programs for patients. Over the last ten years, several research have sought to improve the results of cancer screening in the early stages by employing histopathological pictures and biomarkers, including CA-125 and HE-4 [4]. CA-125 exhibits low precision and specificity in identifying ovarian cancer at its early stages, whereas imaging techniques like CT, US, and MRI are frequently employed to locate and identify characteristics of masses. Nevertheless, the analysis of pictures by skilled radiographers can be a lengthy process and susceptible to differences in interpretation among observers [5]. Recent research has prioritized the utilization of machine learning algorithms to forecast and detect ovarian cancer at an early stage. Various techniques have been suggested for extracting characteristics from ultrasound pictures and categorizing ovarian cancers. Several approaches that can be used include Support Vector Machines (SVM), classifiers based on shallow neural networks, and filters based on wavelet transforms. The extracted features from the images include textured and pathogenic features, polynomial values, uniformity histogram, which as well as dark grey variance multi-scaling. Subsequently, these characteristics are combined using a support-vector-machine (SVM) method to accurately categorize all categories of complete tumors [6].

Belal et. al developed an extensive method to categorize cancer of the uterus by integrating gene expression data with clinical information, so creating a unified strategy for categorizing cancer stage. The rate of classification of Boosting and Ensemble SVM was 80%, whilst other machine learning classifiers had a lower accuracy of 70.77%. The suggested technique exhibited high values for recall, specificity, accuracy, F measure, and AUC [7]. A computer-aided design (CAD) technique to diagnose moderate ovarian cancer by examining S-HG pictures. The researchers employed a k-NN classifier together with a technique for optimization known as T-POT, yielding a mean accuracy ranging from 0.976 to 0.96. A T-POT forecast achieved a predictive accuracy rating of 0.97 and the suggested as a way to obtain high-resolution images of the whole organ while also capturing certain indicators that are not detectable using MPM. Radiation and a model based on CNN in order to make a prediction about endometrioid cancer that shown promising therapeutic potential, despite the fact that the sample size was very small [9].

The MTDL approach may be used to improve classification accuracy and solve challenges related to high-dimensional feature spaces. Additionally, there is the possibility that this method could be used to new dataset categories. There have been a number of studies that have offered promising ways for detecting and forecasting gynaecological malignancies, such as ovarian and endometrial cancers [10]. Utilizing gene expression data, this study employs advanced deep learning and machine learning approaches to cluster and classify ovarian cancer subtypes [11]. Through the integration of ALO-optimized the LSTM technique and CNN networks, a deep learning model that combines the two is proposed. This model makes use of multiple modalities of data, namely gene and histopathology images. Using a hybrid growing deep neural networks model that incorporates a variety of data sources and a large number of assessment markers, the objective is to arrive at a diagnosis of ovarian cancer. In the study, the effectiveness of the suggested method is evaluated in comparison to other different hybrid fused models that have been used in the past. [12].

As opposed to advanced ovarian cancer, peritoneal tuberculosis (TBP) has symptoms that are akin to those of advanced cancer of the ovaries. About one percent to two percent of every case of tuberculosis are caused by TBP. The resemblance among TBP and cancer of the ovary poses difficulties in distinguishing between the two conditions [13]. The process of developing and validating MIA3G, an advanced neural network-based algorithm designed to identify ovarian cancer. The method underwent training using a dataset consisting of 1067 samples and was then verified using a distinct set of 2000 samples. The findings indicate that MIA3G has a sensitiveness of 89.8% and an accuracy of 84.02% for the detection of cancers of the ovary [14].

TABLE I. PREVIOUS STUDIES

Author	*Methods*	*Contribution*	*Limitation*
Danaee et al. [6]	Deep learning	Cancer detection and relevant gene identification	High computational cost and requires large datasets for training
El-Bendary & Belal [7]	Clinical and gene expression integrative approach	Epithelial ovarian cancer stage subtype classification	Lower accuracy (70.77%) with some machine learning classifiers; requires extensive data integration
Wang et al. [8]	Utilizing second-harmonic generation visuals for machine learning purposes.	Detecting early ovarian cancer among individuals without delay	Requires high-quality imaging equipment and expertise in image analysis
Zhang et al. [9]	CNN-based model	Intelligent recognition and prediction of endometrial cancer	Small sample size; limited generalizability
Liao et al. [10]	Multi-task deep convolutional neural network	Cancer diagnosis	High computational complexity; requires large labeled datasets
Guo et al. [11]	Deep learning with multi-omics data	Ovarian cancer subtypes identification	Data heterogeneity; integration challenges with multi-omics data
Ghoniem et al. [12]	Multi-modal evolutionary deep learning model	Ovarian cancer diagnosis	High computational requirements; complexity in model training and optimization
Arezzo et al. [13]	Radiomics analysis	Review on radiomics analysis in ovarian cancer	Challenges in distinguishing peritoneal tuberculosis from advanced ovarian cancer; variability in imaging data quality
Reilly et al. [14]	Algorithm based on deep neural networks (MIA3G)	Validation of algorithm for adnexal mass clinical management	Sensitiveness of 89.8% and accuracy of 84.02%; potential for false positives and negatives
Guo et al. [11]	Deep learning with multi-omics data	Ovarian cancer subtypes identification	Data heterogeneity; integration challenges with multi-omics data

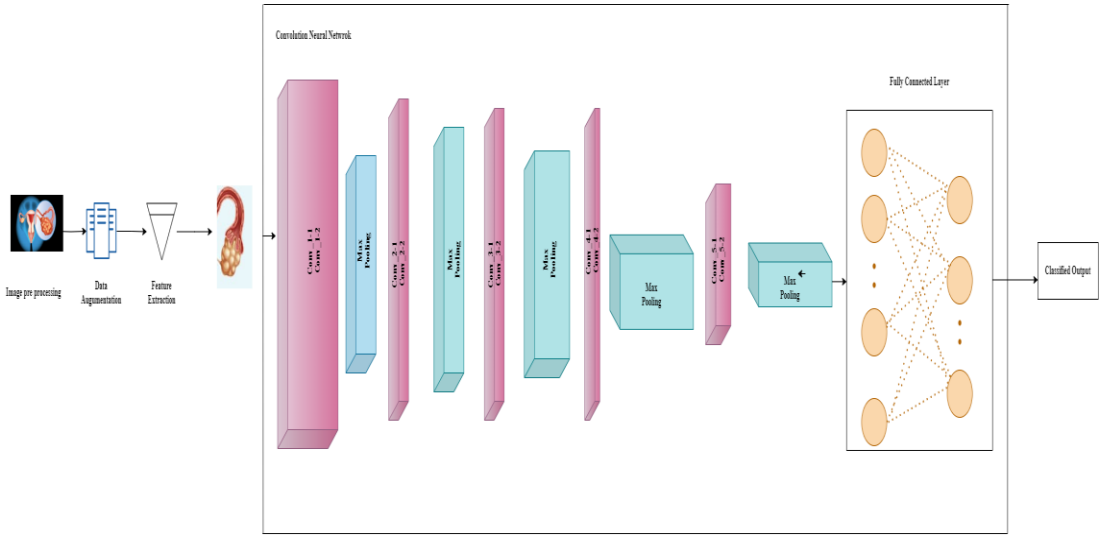

Fig. 1. The Architecture of DeepOva Model

III. METHODOLOGY

The purpose of this part is to present an overview of the methodology that was utilized in the research, which covers the collection of the dataset as well as the proposed design of the CNN [15]. In this experiment, the collection of data that was employed consists of two hundred photos, which are uniformly distributed as follows: one hundred photographs of superficial ovarian cancer and one hundred images of non-cancerous samples. The Cancer Genome Atlas TCGA database was used to generate the original data set, which was subsequently enhanced with 11,040 photos to maximize the platform's deep learning capabilities. 80% of the dataset was designated for training, while 20 % was put aside for testing. The extracted dataset was subsequently utilized for the convolution procedure. The images offered were subjected to a pretreatment process that entailed the elimination of any images that were inadequate, such as those that were converted wrongly and lacked the jpg format extension. The data underwent a cleaning process to eliminate the photos that were distorted. Convolution is a mathematical operation that is used to extract a certain characteristic from a set of inputs. This is done by applying a set of feature detectors, also known as kernels, to the inputs. A tensor is a series of numbers that represents the inputs. The connection between each component of the kernel and the tensor that is being input is calculated separately in each region of the tensor. These calculations are then combined to determine the resulting quantity in the corresponding region of the output tensor, which is called the feature map. Which activation function to use is based on the fact that it does not simultaneously activate all neurons and does not uniformly excite all neurons. Therefore, not all neurons are engaged throughout the process of backpropagation. Subsequently, the data was transmitted through the pooled layer, which employed a conventional down-sampling technique to decrease the size of the feature map elements. This down sampling allowed for increased

flexibility in detecting small shifts and distortions, while also reducing the number of parameters that needed to be learnt in the future layers.

TABLE I. HYPERPARAMETERS FOR DEEPOVA MODEL

S.No	Hyperparameter	Value
1.	Convolutional layers	4
2	Kernel size	5 × 5
3	Type of Pooling	Max pooling
4	Size of Pooling	5*5
5	Filters	32, 64
6	Fully connected	128
7	Activation function	Relu
8	Output of the activation functiont	Sigmoid
9	Loss function	Cross-entropy
10	Optimizer	Adam
11	Rate of learning	0.001

The study employed the technique of Max-pooling. Subsequently, the data was inputted into the flattening layer, where it was transformed into an array with one dimension or vector of integers. In the subsequent step, this array was transmitted as an input to the second layer that was completely combined. Following that, the information is introduced into the completely linked layer of neural networks that are feedforward. Any node in a lower layer is connected to the cells in the one directly above it with adjustable weights, which may be adjusted throughout the learning process. The characteristics acquired from the pooling stages are linked to the outputs of the network. Finally, the outcome was sent to the result layer, where SoftMax was employed for categorization. In this study, the loss function that was utilized was connect entropy as which was determined by the ensuing formula for classifying binary data, which formally follows the equation 1.

$$lf = -(yb \log(pi) + (1 - yb) \log(1 - pi)) \quad (1)$$

Where,

$lf - Loss\ function$

$yb - Binary\ Classification$

$pi - Prediction\ Probability$

A summary of the hyperparameters that are used in the CNN architecture [16] is provided in Table 1.

An analysis is conducted in each tensor area to calculate the element-wise product among every kernel component with the input vector. The computation is combined to determine the resulting value in the corresponding outgoing tensor area, which is reflected by the characteristic maps. Considering stride and padding, Equation 2 was utilized to compute the size of the produced image.

$$\text{OID} = \left[\frac{in + 2p - f}{st} + 1\right] \times \left[\frac{in + 2p - f}{st} + 1\right] \quad (2)$$

Where

in -Input Pixel

p – Padding

f -filter

st-stride

OID- Output Image Dimensions

The nonlinear activation function, technically represented as Equation 3, was given the convolutional result in order to simulate the mathematical behavior of actual neurons.

$$ff(x) = \max(0, x) \quad (3)$$

IV. RESULTS AND DISCUSSION

The dataset consisted of 12,040 images, which were used to train the model. contains an equal number of healthy cells and cells that have been infected with the epithelial cancer group. In order to tune the hyperparameters, the number of epochs was chosen, and the amount was raised by fifty percent increments. The correctness of both the training and validation sets was documented. The procedure of testing was carried out once the training phase was completed. This was accomplished by uploading a image from the evaluation dataset, and the method would then provide the proportion of the image that included both effusion or normal cells. The Xception network succeeds in obtaining good training as well as validation reliability with a minimum number of intervals, as proven by this result, which shows the superiority of the Xception network. It is important to note that this particular type of network does not carry out channel-wise convolution in contrast to conventional generic convolutional neural networks. As a consequence of this, the number of associations is decreased, and the actual weight of the model is decreased. Consequently, it is possible to reach an exceptional level of accuracy with just 50 epochs. Figure 1 and 2 illustrates the model loss and accuracy.

$$\begin{aligned} \text{Overall Accuracy} &= \frac{\text{TP+TN}}{\text{TP+TN+FP+FN}}, \\ \text{Precision} &= \frac{\text{TP}}{\text{TP+FN}}, \\ \text{Recall} &= \frac{\text{TP}}{\text{TP+FP}}, \\ f_1\text{-Score} &= 2 \cdot \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}, \end{aligned} \quad (2)$$

Accuracy: Proportion of correct predictions, broadly indicating model fitness. However, it can be misleading in imbalanced datasets, favoring the majority class.

Precision: Represents the proportion of predictions for a class that are actually correct for that class. High precision means the model rarely makes false positives.

Recall: Represents the proportion of actual positive cases that were correctly identified by the model. High recall means the model rarely misses true positives.

F1-Score: Harmonic mean of precision and recall, rewarding models that excel in both. A good balance between precision and recall is ideal in equation 2. Figure 4 illustrates the comparison Diagnostic Methods for Ovarian Cancer.

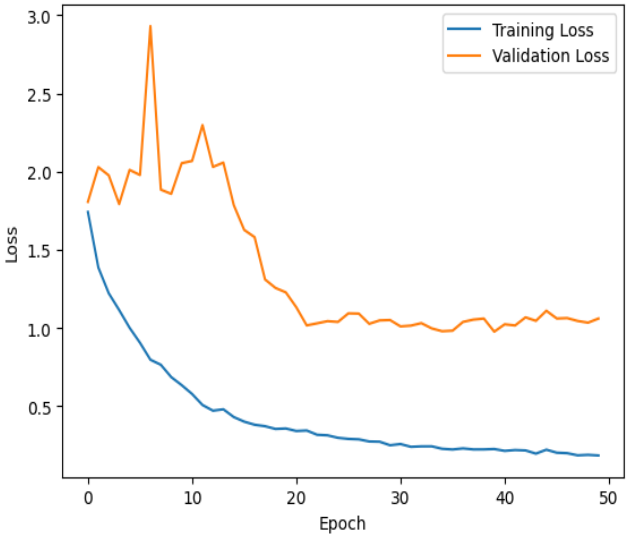

Fig. 2. Model loss

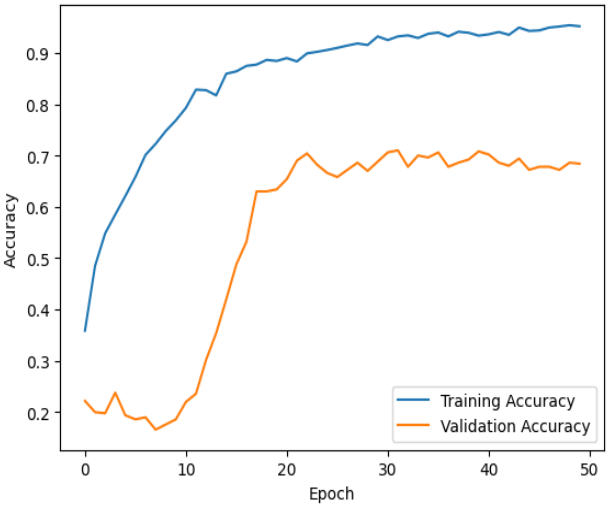

Fig. 3. Model Accuracy.

The suggested CNN, especially when employing the Xception design, exhibited enhanced reliability in training and validation while requiring a limited number of epochs, resulting in an impressive accuracy of 96%. Unlike conventional convolutional neural networks, this architecture eliminates channel-wise convolution, thus decreasing the model's overall weight and the number of connections.

This research introduces a Convolutional Neural Network (CNN) aimed at improving the accuracy and efficiency of diagnostic processes. The CNN, which was trained on histopathology images, achieved a high accuracy rate of 96%.

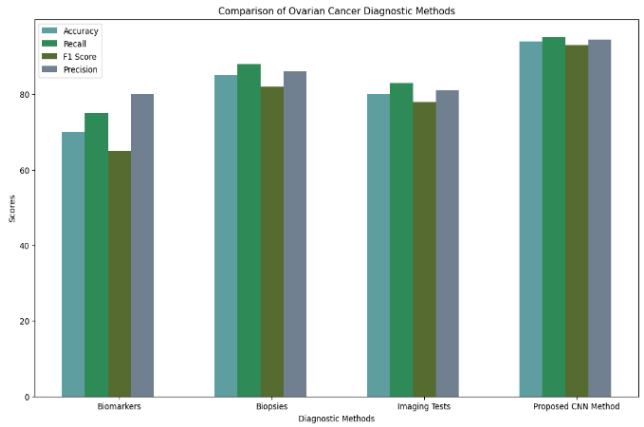

Fig. 4. Comparison of Diagnostic Methods for Ovarian Cancer.

V. CONCLUSION

Ovarian cancer is a prominent contributor to women's cancer-related mortality, primarily because it is often diagnosed at an advanced stage due to the presence of non-specific early symptoms. Existing diagnostic techniques, such as indicators of health, tissue samples, and scans, are plagued by issues of personality, inconsistency across observers, and long methods. This research presents a CNN as a means to enhance the precision and efficiency of diagnostic procedures. The CNN, which underwent training using histopathology pictures, obtained an impressive accuracy rate of 96%. It successfully detected 97.12% of malignant instances and accurately categorized 95.02% of healthy cells. As a result, the CNN significantly reduced both human error and the time required for evaluation. The results highlight the capability of CNN-based frameworks to provide a more accurate, efficient, and dependable approach for detecting ovarian cancer, enhancing the rates of early detection, and subsequently improving patient outcomes. Subsequent investigations will prioritize several crucial domains to better optimize the CNN-based diagnostic tool. The use of recent developments in deep learning, such as transfer learning and reinforcement learning, will enhance the performance of the model. Increasing the scale and variety of the dataset will enhance the ability of the model to apply to various demographics and clinical environments.

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